L Number	Hits	Search Text	DB	Time stamp
1	6879	affinity adj column	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:28
2	399009	sds	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:28
3	12734	mass adj spectr$	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:29
4	1043	(affinity adj column) same sds	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:29
6	0	(mass adj spectr$) same ((affinity adj column) same sds)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:29
5	25	(mass adj spectr$) and ((affinity adj column) same sds)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:42
7	40695	proteome or genome	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:42
8	2870	(affinity adj column) and (proteome or genome)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:42
9	94	(mass adj spectr$) and ((affinity adj column) and (proteome or genome))	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:47
10	707	lc adj ms	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:47
11	0	(affinity adj column) same (lc adj ms)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:48
13	23293	affinity adj chromat$	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:50
14	1	(lc adj ms) same (affinity adj chromat$)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:48
15	1	(affinity adj chromat$) and ((lc adj ms) same (affinity adj chromat$))	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:50
12	32	(affinity adj column) and (lc adj ms)	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:50
-	17693	water adj purification	USPAT; US-PGPUB; EPO; DERWENT	2003/01/27 13:28
-	128916	household or residence	USPAT; US-PGPUB; EPO; DERWENT	2002/05/21 14:57

L7 ANSWER 18 OF 65 MEDLINE DUPLICATE 18
TI Identification of a novel beta-catenin-interacting protein.
AB Cadherin is a well-known cell-cell adhesion molecule, and it binds to beta-catenin, which in turn binds to alpha-catenin. However, little is known about the regulatory mechanism underlying the cadherin-mediated cell-cell adhesion. Here we purified two novel beta-catenin-interacting proteins with molecular masses of 180 kDa (p180) and 150 kDa (p150) from bovine brain cytosol by using glutathione S-transferase (GST)-beta-catenin **affinity column** chromatography. **Mass spectral** analysis revealed p180 to be identical to KIAA0313 which has a putative Rap1 guanine nucleotide exchange factor (GEF) domain and p150 to be the same as KIAA0705 which has a high degree of sequence similarity to the synaptic scaffolding molecule (S-SCAM), which binds beta-catenin and KIAA0313 in the yeast two-hybrid system and overlay assay, respectively (Ide et al., Biochem. Biophys. Res. Commun. 256, 456-461, 1999; Ohtsuka et al., Biochem. Biophys. Res. Commun. 265, 38-44, 1999). beta-Catenin was coimmunoprecipitated with KIAA0313 in Madin-Darby canine kidney II (MDCKII) cells, bovine brain cytosol, and EL cells. KIAA0313 and beta-catenin were partly colocalized at sites of cell-cell contact in MDCKII cells. Taken together, our data suggest that KIAA0313 associates with beta-catenin through KIAA0705 in vivo at sites of cell-cell contact.

SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Jul 5) 273 (2) 712-7.
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AU Kawajiri A; Itoh N; Fukata M; Nakagawa M; Yamaga M; Iwamatsu A; Kaibuchi K

L7 ANSWER 24 OF 65 MEDLINE

TI Use of mass spectrometry to study signaling pathways.

AB Activation of cells by extracellular stimuli, such as growth factors, initiates a cascade of events involving posttranslational modifications, including phosphorylation, formation of protein complexes, and induction or repression of gene expression. Traditionally, genetic methods or specific biochemical assays have been used to identify molecules involved in signaling pathways. Lately, **mass spectrometry**, combined with elegant biochemical approaches, has become a powerful tool for identifying proteins and posttranslational modifications. With this protocol, we hope to bridge the gap between the biochemical and molecular aspects of signal transduction pathways and the **mass spectrometric** tools and techniques that are available to study them. We provide methods for large-scale cell culture and immunoprecipitation of tyrosine-phosphorylated proteins, silver staining of gels, trypsin digests, and protein identification by matrix-assisted laser desorption/ionization (MALDI) **mass spectrometry** and nanoelectrospray tandem **mass spectrometry**. We discuss the special requirements for the identification of phosphorylation sites in proteins by **mass spectrometry**. We describe enrichment of phosphopeptides from unseparated peptide mixtures by immobilized metal **affinity column** (IMAC) and the use of phosphatases to identify phosphorylated peptides. We also discuss specialized methods, such as precursor ion scanning in the negative mode and direct sequencing of phosphopeptides in the positive mode. Our goal is to provide detailed methods in use today for proteomic applications in general and for receptor-mediated signaling pathways in particular.

SO Sci STKE, (2000 Jun 20) 2000 (37) PL1.
Journal code: 100964423. ISSN: 1525-8882.

AU Pandey A; Andersen J S; Mann M